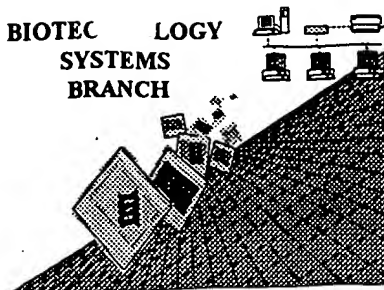


BEST AVAILABLE COPY

BIOTEC  
SYSTEMS  
BRANCH

LOGY



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/784,810

Source: OIPF

Date Processed by STIC: 3/2/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/784,810

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8      Skipped Sequences (OLD RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences (NEW RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10      Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism (NEW RULES)      Sequence(s)      are missing this mandatory field or its response.
- 12      Use of <220>Feature (NEW RULES)      Sequence(s)      are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted "file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 03/02/2001

PATENT APPLICATION: US/09/784,810

TIME: 13:40:11

Input Set : A:\10716-71.app

Output Set: N:\CRF3\03022001\I784810.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Curagen  
 4 RASTELLI, LUCA  
 6 <120> TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING  
 7 SAME  
 9 <130> FILE REFERENCE: 10716-7  
 11 <140> CURRENT APPLICATION NUMBER: US/09/784,810  
 12 <141> CURRENT FILING DATE: 2001-02-14  
 14 <150> PRIOR APPLICATION NUMBER: 60/182,360  
 15 <151> PRIOR FILING DATE: 2000-02-14  
 17 <150> PRIOR APPLICATION NUMBER: 60/191,261  
 18 <151> PRIOR FILING DATE: 2000-03-22  
 20 <160> NUMBER OF SEQ ID NOS: 15  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1600  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 29 <400> SEQUENCE: 1  
 W--> 30 ccccccggg gctcctatag ccacggctcc gggcggggaa ggcgagcccc acagccggcc 60  
 31 ctgcgacgcc cgcctgggca gcaccgataa ggagctgaag gcaggagccg ccgccacggg 120  
 32 cagcgccccc acagcgccag ggacccccctg gcagcgggag ccgcgggtcg aggttatgga 180  
 33 tccagcgggc ggcccccggg gcgtgctccc gcggccctgc cgcgtgctgg tgctgctgaa 240  
 34 ccgcgcgggc ggcaagggca aggccttgca gctcttcgg agtcacgtgc agcccctttt 300  
 35 ggctgaggct gaaatctcct tcacgctgat gctcactgag cggcggaacc acgcgcggga 360  
 36 gctgggtgcg tcggaggagc tgggcccgtg ggacgctctg gtggtcatgt ctggagacgg 420  
 37 gctgatgcac gaggtggtga acgggctcat ggagcggcct gactgggaga ccgccatcca 480  
 38 gaagcccctg tgtagcctcc cagcaggctc tggcaacgcg ctggcagctt ccttgaacca 540  
 39 ttatgctggc tatgagcagg tcaccaatga agacctcctg accaactgca cgctattgct 600  
 40 gtgcgcgccg gtgctgtcac ccatgaacct gctgtctctg cacacggctt cggggctgcg 660  
 41 ctgcttctct gtgctcagcc tggcctgggg cttcattgct gatgtggacc tagagagtga 720  
 42 taagtatcgg cgtctggggg agatgcgctt cactctgggc accttcctgc gtctggcagc 780  
 43 cctgcgcacc taccgcgccc gactggctac cctccctgta ggaagagtgg gtttcaagac 840  
 44 acctgcttcc ccggttggtg tccagcaggg ccggttagat gcacacctgg tgccactgga 900  
 45 ggagcaggtg ccttctcact ggcaggtggt gcccgacgag gactttgtgc tagtcctggc 960  
 46 actgctgcac tcgcacctgg ccagtgcgat gtttgcgtgca cccatgggcc gctgtgcagc 1020  
 47 tggcgtcatg catctgttct acgtgcgggc gggagtgtct cgtgccatgc tgctgcgcct 1080  
 48 ctctctggcc atggagaagg gcaggcatat ggagtatgaa tgcccctact tggatatatg 1140  
 49 gcccggtggt gccttcgctc tggagcccaa ggatgggaaa ggtgtgtttg cagtggatgg 1200  
 50 ggaattgatg gttagcgagg ccgtgcaggg ccaggtgcac ccaaactact tctggatggt 1260  
 51 cagcgggttg gtggagcccc cgcacagctg gaagcccag cagatgccac cgccagaaga 1320  
 52 gcccttatga cccctgggcc gcgctgtgcc ttagtgtcta cttgcaggac ccttcctcct 1380  
 53 tccctagggc tgcagggcct gtccacagct cctgtggggg tggaggagac tcctctggag 1440  
 54 aaggggtgaga aggtggaggc tatgctttgg ggggacaggc cagaatgaag tcctgggtca 1500  
 55 ggagcccagc tggctgggcc cagctgccta tgtaaggcct tctagtttgt tctgagacct 1560  
 56 ccaccccacg aaccaaattc aaataaagtg acattcccaa 1600  
 59 <210> SEQ ID NO: 2  
 60 <211> LENGTH: 384

*see item 10 on Error Summary Sheet*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/784,810

DATE: 03/02/2001  
 TIME: 13:40:11

Input Set : A:\10716-71.app  
 Output Set: N:\CRF3\03022001\I784810.raw

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61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
65 Met Asp Pro Ala Gly Gly Pro Arg Gly Val Leu Pro Arg Pro Cys Arg
66   1          5          10          15
68 Val Leu Val Leu Leu Asn Pro Arg Gly Gly Lys Gly Lys Ala Leu Gln
69          20          25          30
71 Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser
72          35          40          45
74 Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
75          50          55          60
77 Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
78  65          70          75          80
80 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
81          85          90          95
83 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
84          100          105          110
86 Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
87          115          120          125
89 Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg
90          130          135          140
92 Pro Val Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
93 145          150          155          160
95 Leu Arg Ser Phe Ser Val Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp
96          165          170          175
98 Val Asp Leu Glu Ser Asp Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe
99          180          185          190
101 Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly
102          195          200          205
104 Arg Leu Ala Thr Leu Pro Val Gly Arg Val Gly Phe Lys Thr Pro Ala
105          210          215          220
107 Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro
108 225          230          235          240
110 Leu Glu Glu Gln Val Pro Ser His Trp Gln Val Val Pro Asp Glu Asp
111          245          250          255
113 Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Ala Ser Glu Met
114          260          265          270
116 Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe
117          275          280          285
119 Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu
120          290          295          300
122 Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val
123 305          310          315          320
125 Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro Lys Asp Gly Lys Gly
126          325          330          335
128 Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly
129          340          345          350
131 Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro
132          355          360          365

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/784,810

DATE: 03/02/2001

TIME: 13:40:11

Input Set : A:\10716-71.app

Output Set: N:\CRF3\03022001\I784810.raw

```

134 Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro Pro Glu Glu Pro Leu
135      370      375      380
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 1759
143 <212> TYPE: DNA
144 <213> ORGANISM: Mus musculus
146 <400> SEQUENCE: 3
147 gaactccagg gtcctctggg agagaagcca ccttcaaggc gtgacctagt tcactgcaat 60
148 cctttcttat ctgggttcgt ttctctcttg gactcgcttc ttctggactt taagaagcga 120
149 tgcgaagata gagatctggc cgccccgggg aatgacgagg gcgctcacac agcccaggga 180
150 ggtggagagg gcgagcccac ggccagtcgc cagacaccct cctgggcaac accgataaga 240
151 agctgaacgc aggagccgcc gttacctcta gcagcgccgg ggcagaccgg gtggccctt 300
152 gtcagcgagg gccccgggac ctggctatgg aaccagtaga atgccctcga ggactgctcc 360
153 cacggccatg cagagtgtgt gtgtgtgtga acccccaggg tggcaagggc aaggctctgc 420
154 agctcttcca gagcgtgtgt cagcccttcc tggaggaggc agagataacc tttaaactga 480
155 tactcaccga acggaagaac catgccaggg agctgggtgt tgcagaggag ttgggtcact 540
156 gggacgcctt ggagtcctgt tccggtgatg gtctgatgca tgaagtgggt aatgggctaa 600
157 tggaaaggcc agactgggag actgccatcc agaaaccctt gtgtagcctc cctggagggt 660
158 ccggcaatgc gctggcagct tctgtgaacc actatgctgg gtacgagcag gtgactaatg 720
159 aagacctgct catcaactgc acactgctgt tgtgcccgcg gcgctgtca cccatgaacc 780
160 tgctgtccct gcacactgct tctgggctgc ggctctatc tgtgtcagt ctgtcctggg 840
161 gctttgttgc tgacgtggac ctcgagagtg agaagtacag gcgcttgggg gagattcgtt 900
162 tcacagtggg caccttcttt cgcctagcaa gcctgcgcat ctaccaaggc caactggcct 960
163 accttctctg aggaactgtg gcctctaaga gaccgcctc tacactggtg cagaagggcc 1020
164 ccgtcgacac acaccttgtt cctctggagg agccagtgcc ttctcattgg actgtggtac 1080
165 cagaacagga ctctgtctgt gtgtgtgtgc tgctacacac ccacctgagc tccgagctgt 1140
166 ttgcagcacc catgggcccgc tgtgaggctg gtgttatgca tctgttctac gtacgtgagg 1200
167 ggggtgtcaag ggctgcgctg ctgcgcctct tcctggccat gcagaagggc aagcataatg 1260
168 aacttgactg tccatactgt gttcatgtgc ccgtgggtgc ttccgcctg gagcccagga 1320
169 gccagagggg cgtgttttct gtggatggag agctgatggg atgtgaagct gtgcagggcc 1380
170 aagtgcaccc aaactacctt tggatgggtc gtggcagcag aatgccccca tccggccggg 1440
171 actcccggcg ggggccacct ccagaagaac cataactctg tgcctttgtc tactctgtct 1500
172 aggtgagatg gggaccctcc ccgcaccca cctcctggta tgggagggtt tttctaaagt 1560
173 tcctatggaa gtgggtggga cccctgcaga gaaagctaga aggtggggct atgacttggg 1620
174 aagaaaggct ttaccttcca gttagagtaa catccccagt agagccctgc tggctggacc 1680
175 agttgcatat agaagacatt cccattgct tttagggacc ttccctggga accaaattca 1740
176 aataaagaga cttttccaa 1759
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 382
181 <212> TYPE: PRT
182 <213> ORGANISM: Mus musculus
184 <400> SEQUENCE: 4
185 Met Glu Pro Val Glu Cys Pro Arg Gly Leu Leu Pro Arg Pro Cys Arg
186      1      5      10      15
188 Val Leu Val Leu Leu Asn Pro Gln Gly Gly Lys Gly Lys Ala Leu Gln
189      20      25      30
191 Leu Phe Gln Ser Arg Val Gln Pro Phe Leu Glu Glu Ala Glu Ile Thr
192      35      40      45
194 Phe Lys Leu Ile Leu Thr Glu Arg Lys Asn His Ala Arg Glu Leu Val

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/784,810

DATE: 03/02/2001

TIME: 13:40:11

Input Set : A:\10716-71.app

Output Set: N:\CRF3\03022001\I784810.raw

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195      50      55      60
197 Cys Ala Glu Glu Leu Gly His Trp Asp Ala Leu Ala Val Met Ser Gly
198 65      70      75      80
200 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
201      85      90      95
203 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Gly Gly Ser
204      100      105      110
206 Gly Asn Ala Leu Ala Ala Ser Val Asn His Tyr Ala Gly Tyr Glu Gln
207      115      120      125
209 Val Thr Asn Glu Asp Leu Leu Ile Asn Cys Thr Leu Leu Leu Cys Arg
210      130      135      140
212 Arg Arg Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
213 145      150      155      160
215 Leu Arg Leu Tyr Ser Val Leu Ser Leu Ser Trp Gly Phe Val Ala Asp
216      165      170      175
218 Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Ile Arg Phe
219      180      185      190
221 Thr Val Gly Thr Phe Phe Arg Leu Ala Ser Leu Arg Ile Tyr Gln Gly
222      195      200      205
224 Gln Leu Ala Tyr Leu Pro Val Gly Thr Val Ala Ser Lys Arg Pro Ala
225      210      215      220
227 Ser Thr Leu Val Gln Lys Gly Pro Val Asp Thr His Leu Val Pro Leu
228 225      230      235      240
230 Glu Glu Pro Val Pro Ser His Trp Thr Val Val Pro Glu Gln Asp Phe
231      245      250      255
233 Val Leu Val Leu Val Leu Leu His Thr His Leu Ser Ser Glu Leu Phe
234      260      265      270
236 Ala Ala Pro Met Gly Arg Cys Glu Ala Gly Val Met His Leu Phe Tyr
237      275      280      285
239 Val Arg Ala Gly Val Ser Arg Ala Ala Leu Leu Arg Leu Phe Leu Ala
240      290      295      300
242 Met Gln Lys Gly Lys His Met Glu Leu Asp Cys Pro Tyr Leu Val His
243 305      310      315      320
245 Val Pro Val Val Ala Phe Arg Leu Glu Pro Arg Ser Gln Arg Gly Val
246      325      330      335
248 Phe Ser Val Asp Gly Glu Leu Met Val Cys Glu Ala Val Gln Gly Gln
249      340      345      350
251 Val His Pro Asn Tyr Leu Trp Met Val Cys Gly Ser Arg Asp Ala Pro
252      355      360      365
254 Ser Gly Arg Asp Ser Arg Arg Gly Pro Pro Pro Glu Glu Pro
255      370      375      380
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 1840
260 <212> TYPE: DNA
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 5
264 gccggcgccc ccggcgcgga tgccctgctct gtgcctgtat ctgagatcat cgccgttgag 60
265 gaaacagacg ttcacgggaa acatcaaggc agtgaaaaat ggcagaaaat ggaaaagcct 120
266 tacgctttta cagttcactg tgtaaaagaga gcacgacggc accgctggaa gtgggcgcag 180

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## RAW SEQUENCE LISTING

DATE: 03/02/2001

PATENT APPLICATION: US/09/784,810

TIME: 13:40:11

Input Set : A:\10716-71.app

Output Set: N:\CRF3\03022001\I784810.raw

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267 gtgactttct ggtgtccaga ggagcagctg tgtcacttgt ggctgcagac cctgcgggag 240
268 atgctggaga agctgacgtc cagaccaaag catttactgg tatttatcaa cccgtttgga 300
269 ggaagaggac aaggcaagcg gatatatgaa agaaaagtgg caccactgtt caccttagcc 360
270 tccatcacca ctgacatcat cggtaacaaa ttctatgtta actatgtaga agtaattact 420
271 gaacatgcta atcaggccaa ggagactctg tatgagatta acatagacaa atacgacggc 480
272 atcgtctgtg tcggcggaga tggtagttc agcgaggtgc tgcacgtctt gattgggagg 540
273 acgcagagga gcgcgggggt cgaccagaac caccgccggg ctgtgctggt cccagtagc 600
274 ctccggattg gaatcattcc cgcagggtca acggactgcg tgtgttactc caccgtgggc 660
275 accagcgacg cagaaacctc ggcgtgcac atcgttgttg gggactcgtt ggccatggat 720
276 gtgtcctcag tccaccacaa cagcacactc ctctgctact ccgtgtccct gctgggctac 780
277 ggcttctacg gggacatcat caaggacagt gagaagaaac ggtggttggg tcttgccaga 840
278 tacgactttt caggttttaa gaccttcctc tcccaccact gctatgaagg gacagtgtcc 900
279 ttctccctcg cacaacacac ggtgggatct ccaagggata ggaagccctg ccgggcagga 960
280 tgctttgttt gcaggcaaag caagcagcag ctggaggagg agcagaagaa agcactgtat 1020
281 ggtttggaag ctgcggagga cgtggaggag tggcaagtcg tctgtgggaa gtttctggcc 1080
282 atcaatgcca caaacatgtc ctgtgcttgt cgccggagcc ccaggggcct ctcccggct 1140
283 gccacttggg gagacgggtc ttctgacctc atcctcatcc ggaaatgtc caggttcaat 1200
284 tttctgagat ttctcatcag gcacaccaac cagcaggacc agtttgactt cacttttgtt 1260
285 gaagtattat cgcgaagaa attccagttt acgtcgaagc acatggagga tgaggacagc 1320
286 gacctcaagg agggggggaa gaagcgcttt gggcacattt gcagagcca cccctcctgc 1380
287 tgtgcaccg tctccaacag ctcttggaac tgcgacgggg aggtcctgca cagccctgcc 1440
288 atcgaggtca ggtgccactg ccagctgggt cgactctttg cacgaggaat tgaagagaat 1500
289 ccgaagccag actcacacag ctgagaagcc ggcgtcctgc tcacaaactg ggaaagtgtg 1560
290 aaaactattt aagataatta ttacagacca attatgttga tatatacatt taaatgtaga 1620
291 aatttatttt tgatagttaa atcttgattt tagaagaaaa cccttttgtc aacaattttg 1680
292 tgtacatatt tggcattttc agttctgtac gcactctcgg gttgcagccc acgcccgtta 1740
293 ctctcagcaa gaaagaggtg gaggttgagg tgagccaaga ttgcgccact gcactccagc 1800
294 ctgggcaaac agagggagac tccatgcgcc ccccaacaa 1840

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297 &lt;210&gt; SEQ ID NO: 6

298 &lt;211&gt; LENGTH: 471

299 &lt;212&gt; TYPE: PRT

300 &lt;213&gt; ORGANISM: Homo sapiens

302 &lt;400&gt; SEQUENCE: 6

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303 Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val Lys Arg Ala Arg
304 1 5 10 15
306 Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp Cys Pro Glu Glu
307 20 25 30
309 Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys
310 35 40 45
312 Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly
313 50 55 60
315 Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu
316 65 70 75 80
318 Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr
319 85 90 95
321 Val Asn Tyr Val Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu
322 100 105 110
324 Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val
325 115 120 125

```

## VERIFICATION SUMMARY

DATE: 03/02/2001

PATENT APPLICATION: US/09/784,810

TIME: 13:40:12

Input Set : A:\10716-71.app

Output Set: N:\CRF3\03022001\I784810.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:30 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1  
L:30 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:30 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:30 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1